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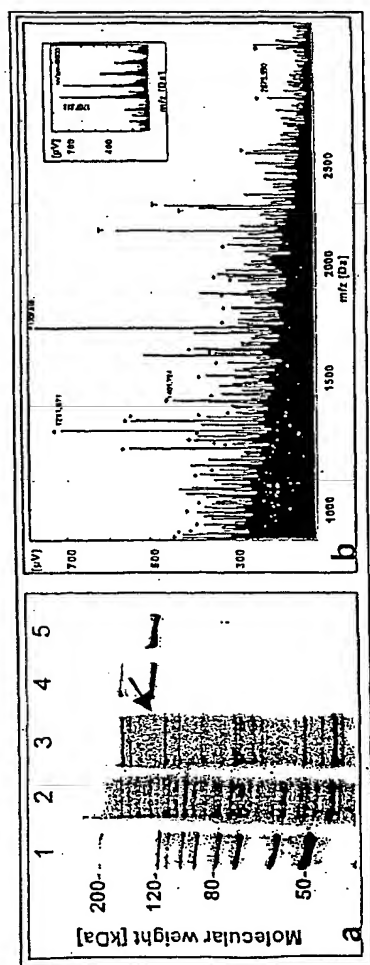


Fig. 1

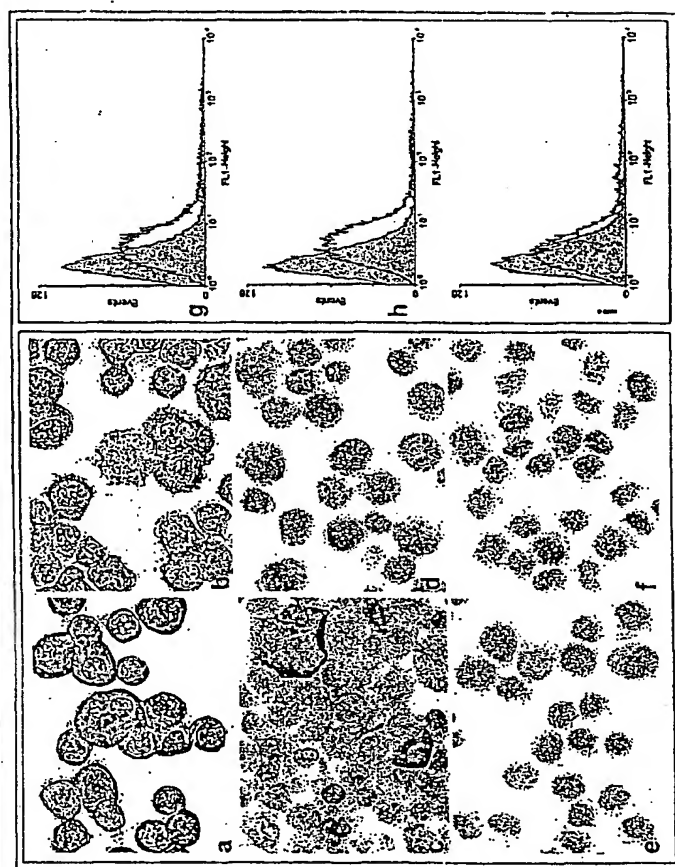


Fig. 2

Fig. 3

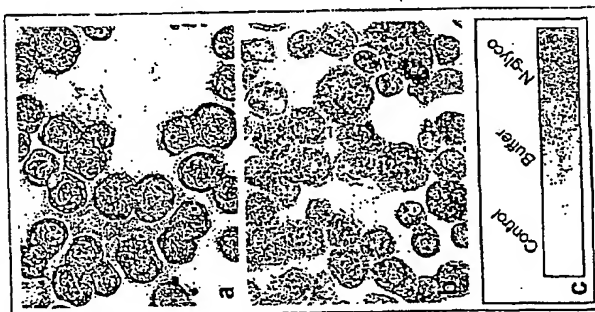


Fig. 4

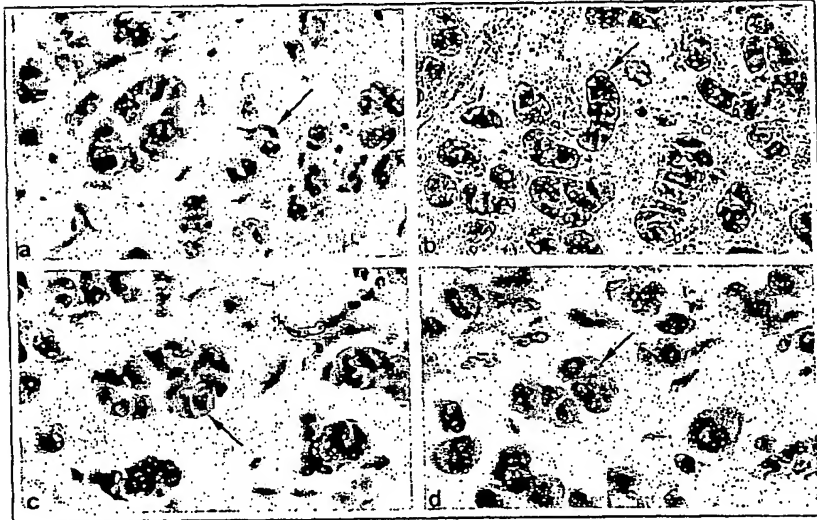


Fig. 5

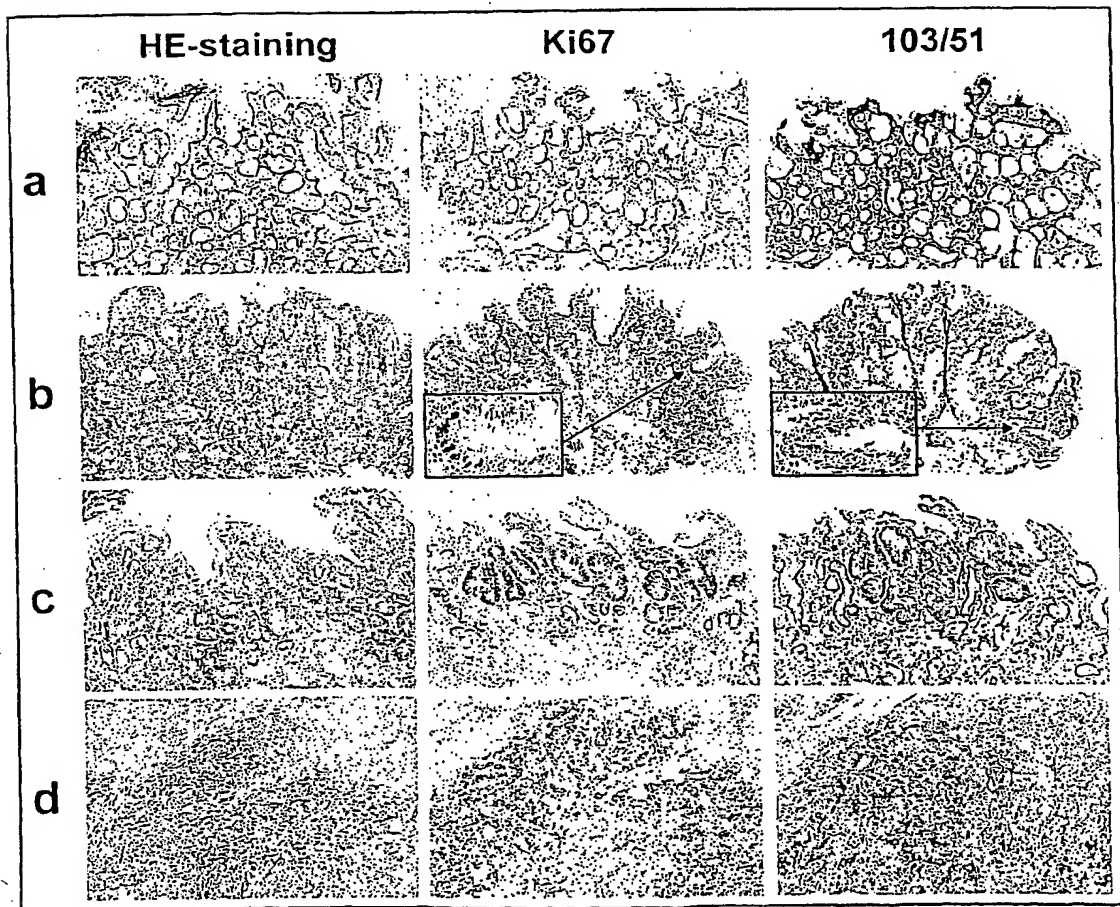


Fig. 6

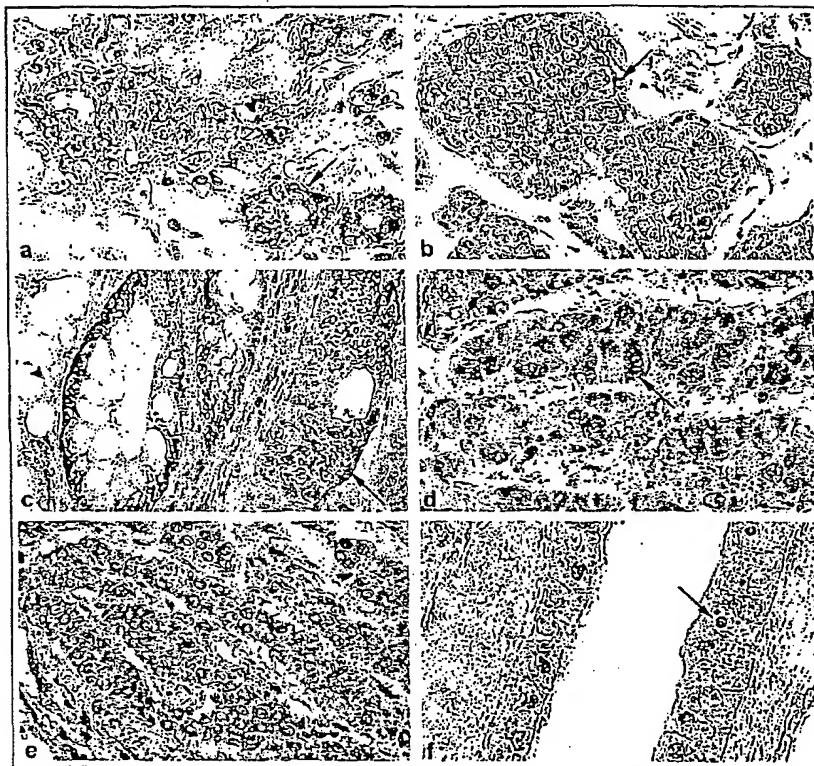
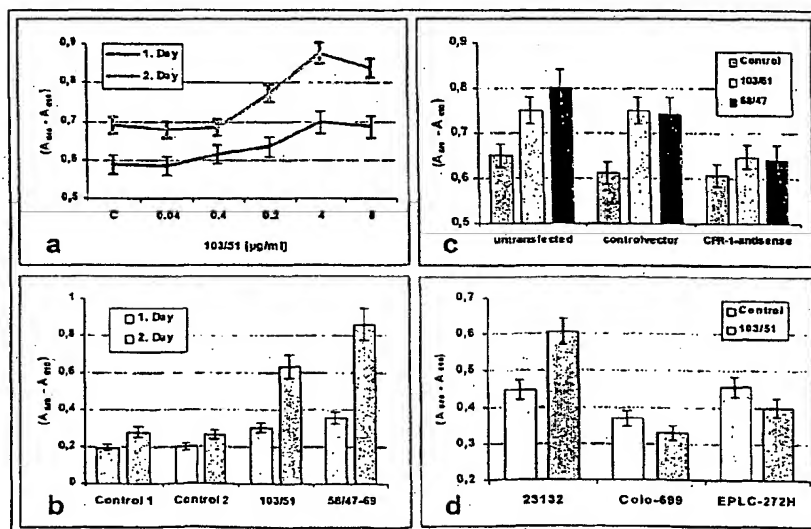


Fig. 7



tcc tgc aag gct tct ggc tac acc ttc act gac tac tat ata aac	45
Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Tyr Ile Asn	
1 5 10 15	
tgg gtg aag cag agg act gga cag ggc ctt gag tgg att gga gag	90
Trp Val Lys Gln Arg Thr Gly Gln Gly Leu Glu Trp Ile Gly Glu	
20 25 30	
att tat cct gga agt ggt aat act tac tac aat gag aag ttc aag	135
Ile Tyr Pro Gly Ser Gly Asn Thr Tyr Tyr Asn Glu Lys Phe Lys	
35 40 45	
ggc aag gcc aca ctg act gca gac aaa tcc tcc agc aca gcc tac	180
Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr	
50 55 60	
atg cag ctc agc agc ctg aca tct gag gac tct gca gtc tat ttc	225
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe	
65 70 75	
tgt gca aga tcg gga tta cga ccc tat gct atg gac tac tgg ggt	270
Cys Ala Arg Ser Gly Leu Arg Pro Tyr Ala Met Asp Tyr Trp Gly	
80 85 90	
caa gga acc tca gtc acc	
Gln Gly Thr Ser Val Thr	
95	

Fig. 8A

Nucleotide sequence of the variable region of the heavy chain (VH) of antibody NM58-49/69

CDR1	
tcc tgc aag gct tct ggc tac acc ttc act gac tac tat ata aac	
Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Tyr Ile Asn	15
1	
tgg gtg aag cag agg act gga cag ggc ctt gag tgg att gga gag	90
Trp Val Lys Gln Arg Thr Gly Gln Gly Leu Glu Trp Ile Gly Glu	30
20	
CDR2	
att tat cct gga agt ggt aat act tac tac aat gag aag ttc aag	135
Ile Tyr Pro Gly Ser Gly Asn Thr Tyr Tyr Asn Glu Lys Phe Lys	45
35	
ggc aag gcc aca ctg act gca gac aca tcc tcc agc aca gcc tac	180
Gly Lys Ala Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr	60
50	
atg cag ctc agc agc ctg aca tct gag gac tct gca gtc tat ttc	225
Met Gln Leu Ser Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe	75
65	
D-gene CDR3 J-gene	
tgt gca aga tcg gga tta cga ccc tat gct atg gac tac tgg ggt	270
Cys Ala Arg Ser Gly Leu Arg Pro Tyr Ala Met Asp Tyr Trp Gly	90
80	
caa gga acc tca gtc acc	
Gln Gly Thr Ser Val Thr	

Fig. 8B

cca ctc tcc ctg cct gtc agt ctt gga gat caa gcc tcc atc tct	45
Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser	
1 5 10 15	
tgc aga tct agt cag agc att gta cat agt aat gga aac acc tat	90
Cys Arg Ser Ser Gln Ser Ile Val His Ser Asn Gly Asn Thr Tyr	
20 25 30	
tta gaa tgg tac ctg cag aaa cca ggc cag tct cca aag ctc ctg	135
Leu Glu Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu	
35 40 45	
atc tac aaa gtt tcc aac cga ttt tct ggg gtc cca gac agg ttc	180
Ile Tyr Lys Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe	
50 55 60	
agt ggc agt gga tca ggg aca gat ttc aca ctc aag atc agc aga	225
Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg	
65 70 75	
gtg gag gct gag gat ctg gga gtt tat tac tgc ttt caa ggt tca	270
Val Glu Ala Glu Asp Leu Gly Val Tyr Tyr Cys Phe Gln Gly Ser	
80 85 90	
cat gtt ccg tac acg ttc gga ggg ggg acc aag ctg gaa ata aaa	315
His Val Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys	
95 100 105	

Fig. 9A

Nucleotide sequence of the variable region of the light chain (VL) of antibody NM58-49/69

```

cca ctc tcc ctg cct gtc agt ctt gga gat caa gcc tcc atc tct 45
pro leu ser leu pro val ser leu gly asp gln ala ser ile ser
1      5      10      15

tgc aga tct agt cag agc att gta cat agt aat gga aac acc tat 90
cys arg ser ser gln ser ile val his ser asn gly asn thr tyr
20      25      30

tta gaa tgg tac ctg cag aaa cca gcc cag tct cca aag ctc ctg 135
leu glu trp tyr leu gln lys pro gly gln ser pro lys leu leu
35      40      45

atc tac aaa gtt tcc aac cga ttt tct ggg gtc cca agg ttc 180
ile tyr lys val ser asn arg phe ser gly val pro asp arg phe
50      55      60

agt ggc agt gga tca ggg aca gat ttc aca ctc aag atc agc aga 225
ser gly ser gly ser gly thr asp phe thr leu lys ile ser arg
65      70      75

gtg gag gct gag gat ctg gga gtt tat tac tgc ttt caa ggt tca 270
val glu ala glu asp leu gly val tyr tyr cys phe gln gly ser
80      85      90

cat gtt ccg tac acg ttc gga ggg ggg acc aag ctg gaa ata aaa 315
his val pro tyr thr phe gly gly gly thr lys leu glu ile lys
95      100      105

```

Fig. 9B



gat gtg agg gag cct gaa aat gaa att tct tca gac tgc aat cat	45
Asp Val Arg Glu Pro Glu Asn Glu Ile Ser Ser Asp Cys Asn His	
5 10 15	
ttg ttg tgg aat tat aag ctg aac cta act aca gat ccc aaa ttt	90
Leu Leu Trp Asn Tyr Lys Leu Asn Leu Thr Thr Asp Pro Lys Phe	
20 25 30	
gaa tct gtg gcc aga gag gtt tgc aaa tct act ata aca gag att	135
Glu Ser Val Ala Arg Glu Val Cys Lys Ser Thr Ile Thr Glu Ile	
35 40 45	
gaa gaa tgt gct gat gaa ccg gtt gga aaa ggt tac atg gtt tcc	180
Glu Glu Cys Ala Asp Glu Pro Val Gly Lys Gly Tyr Met Val Ser	
50 55 60	
tgc ttg gtg gat cac cga ggc aac atc act gag tat cag tgt cac	225
Cys Leu Val Asp His Arg Gly Asn Ile Thr Glu Tyr Gln Cys His	
65 70 75	
cag tac att acc aag atg acg gcc atc att ttt agt gat tac cgt	270
Gln Tyr Ile Thr Lys Met Thr Ala Ile Ile Phe Ser Asp Tyr Arg	
80 85 90	
tta atc tgt ggc ttc atg gat gac tgc aaa aat gac atc aac att	315
Leu Ile Cys Gly Phe Met Asp Asp Cys Lys Asn Asp Ile Asn Ile	
95 100 105	
ctg aaa tgt ggc agt att cgg ctt gga gaa aag gat gca cat tca	360
Leu Lys Cys Gly Ser Ile Arg Leu Gly Glu Lys Asp Ala His Ser	
110 115 120	
caa ggt gag gtg gta tca tgc ttg gag aaa ggc ctg gtg aaa gaa	405
Gln Gly Glu Val Val Ser Cys Leu Glu Lys Gly Leu Val Lys Glu	
125 130 135	
gca gaa gaa aga gaa ccc aag att caa gtt tct gaa ctc tgc aag	450
Ala Glu Glu Arg Glu Pro Lys Ile Gln Val Ser Glu Leu Cys Lys	
140 145 150	
aaa gcc att ctc cgg gtg gct gag ctg tca tcg gat gac ttt cac	495
Lys Ala Ile Leu Arg Val Ala Glu Leu Ser Ser Asp Asp Phe His	
155 160 165	
tta gac cgg cat tta tat ttt gct tgc cga gat gat cgg gag cgt	540
Leu Asp Arg His Leu Tyr Phe Ala Cys Arg Asp Asp Arg Glu Arg	
170 175 180	
ttt tgt gaa aat aca caa gct ggt gag ggc aga gtg tat aag tgc	585
Phe Cys Glu Asn Thr Gln Ala Gly Glu Gly Arg Val Tyr Lys Cys	
185 190 195	
ctc ttt aac cat aaa ttt gaa gaa tcc atg agt gaa aag tgt cga	630
Leu Phe Asn His Lys Phe Glu Glu Ser Met Ser Glu Lys Cys Arg	
200 205 210	

Fig. 10-1

# Title: Neoplasm-Specific Polypeptides and Their Uses

Applicant(s): Müller-Hermelink et al.

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cgc atg ttg atg gaa gac ttt tct ctg agc cct gag atc atc cta Arg Met Leu Met Glu Asp Phe Ser Leu Ser Pro Glu Ile Ile Leu 290 295 300	900
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aag ggg aac ctt gga atg aac tgc cag cag gcg ctt caa aca ctg Lys Gly Asn Leu Gly Met Asn Cys Gln Gln Ala Leu Gln Thr Leu 335 340 345	1035
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ttg aat gaa gct tgt gaa tct gta atc cag aca gcc tgc aaa cat Leu Asn Glu Ala Cys Glu Ser Val Ile Gln Thr Ala Cys Lys His 365 370 375	1125
ata aga tct gga gac cca atg atc ttg tgc tgc ctg atg gaa cat Ile Arg Ser Gly Asp Pro Met Ile Leu Ser Cys Leu Met Glu His 380 385 390	1170
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gag ctg cag tat ttc atc tcc cgg gat tgg aag ctg gac cct gtc Glu Leu Gln Tyr Phe Ile Ser Arg Asp Trp Lys Leu Asp Pro Val 410 415 420	1260
ctg tac cgc aag tgc cag gga gac gct tct cgt ctt tgc cac acc Leu Tyr Arg Lys Cys Gln Gly Asp Ala Ser Arg Leu Cys His Thr 425 430 435	1305
cac ggt tgg aat gag acc agc gaa ttt atg cct cag gga gct gtg His Gly Trp Asn Glu Thr Ser Glu Phe Met Pro Gln Gly Ala Val 440 445 450	1350
ttc tct tgt tta tac aga cac gcc tac cgc act gag gaa cag gga Phe Ser Cys Leu Tyr Arg His Ala Tyr Arg Thr Glu Glu Gln Gly 455 460 465	1395

Fig. 10-2

agg agg ctc tca cgg gag tgc cga gct gaa gtc caa agg atc cta Arg Arg Leu Ser Arg Glu Cys Arg Ala Glu Val Gln Arg Ile Leu 470 475 480	1440
cac cag cgt gcc atg gat gtc aag ctg gat cct gcc ctc cag gat His Gln Arg Ala Met Asp Val Lys Leu Asp Pro Ala Leu Gln Asp 485 490 495	1485
aag tgc ctg att gat ctg gga aaa tgg tgc agt gag aaa aca gag Lys Cys Leu Ile Asp Leu Gly Lys Trp Cys Ser Glu Lys Thr Glu 500 505 510	1530
act gga cag aag ctg gag tgc ctt cag gac cat ctg gat gac tta Thr Gly Gln Lys Leu Glu Cys Leu Gln Asp His Leu Asp Asp Leu 515 520 525	1575
gtg gtg gag tgt aga gat ata gtt ggc aac ctc act gag tta gaa Val Val Glu Cys Arg Asp Ile Val Gly Asn Leu Thr Glu Leu Glu 530 535 540	1620
tca gag gat att caa ata gaa gcc ttg ctg atg aga gcc tgt gag Ser Glu Asp Ile Gln Ile Glu Ala Leu Leu Met Arg Ala Cys Glu 545 550 555	1665
ccc ata att cag aac ttc tgc cac gat gtg gca gat aac cag ata Pro Ile Ile Gln Asn Phe Cys His Asp Val Ala Asp Asn Gln Ile 560 565 570	1710
gac tcc ggg gac ctg atg gag tgt ctg ata cag aac aaa cac cag Asp Ser Gly Asp Leu Met Glu Cys Leu Ile Gln Asn Lys His Gln 575 580 585	1755
aag gac atg aac gag aag tgt gcc atc gga gtt acc cac ttc cag Lys Asp Met Asn Glu Lys Cys Ala Ile Gly Val Thr His Phe Gln 590 595 600	1800
ctg gtg cag atg aag gat ttt cgg ttt tct tac aag ttt aaa atg Leu Val Gln Met Lys Asp Phe Arg Phe Ser Tyr Lys Phe Lys Met 605 610 615	1845
gcc tgc aag gag gac gtg ttg aag ctt tgc cca aac ata aaa aag Ala Cys Lys Glu Asp Val Leu Lys Leu Cys Pro Asn Ile Lys Lys 620 625 630	1890
aag gtg gac gtg gtg atc tgc ctg agc acg acc gtg cgc aat gac Lys Val Asp Val Val Ile Cys Leu Ser Thr Thr Val Arg Asn Asp 635 640 645	1935
act ctg cag gaa gcc aag gag cac agg gtg tcc ctg aag tgc cgc Thr Leu Gln Glu Ala Lys Glu His Arg Val Ser Leu Lys Cys Arg 650 655 660	1980
agg cag ctc cgt gtg gag gag ctg gag atg acg gag gac atc cgc Arg Gln Leu Arg Val Glu Glu Leu Glu Met Thr Glu Asp Ile Arg 665 670 675	2025
ttg gag cca gat cta tac gaa gcc tgc aag agt gac atc aaa aac Leu Glu Pro Asp Leu Tyr Glu Ala Cys Lys Ser Asp Ile Lys Asn 680 685 690	2070
ttc tgt tcc gct gtg caa tat ggc aac gct cag att atc gaa tgt Phe Cys Ser Ala Val Gln Tyr Gly Asn Ala Gln Ile Ile Glu Cys 695 700 705	2115
ctg aaa gaa aac aag aag cag cta agc acc cgc tgc cac caa aaa Leu Lys Glu Asn Lys Lys Gln Leu Ser Thr Arg Cys His Gln Lys 710 715 720	2160

Fig. 10-3

gta ttt aag ctg cag gag aca gag atg atg gac cca gag cta gac Val Phe Lys Leu Gln Glu Thr Glu Met Met Asp Pro Glu Leu Asp 725 730 735	2205
tac acc ctc atg agg gtc tgc aag cag atg ata aag aag ttc tgt Tyr Thr Leu Met Arg Val Cys Lys Gln Met Ile Lys Lys Phe Cys 740 745 750	2250
ccg gaa gca gat tct aaa acc atg ttg cag tgc ttg aag caa aat Pro Glu Ala Asp Ser Lys Thr Met Leu Gln Cys Leu Lys Gln Asn 755 760 765	2295
aaa aac agt gaa ttg atg gat ccc aaa tgc aaa cag atg ata acc Lys Asn Ser Glu Leu Met Asp Pro Lys Cys Lys Gln Met Ile Thr 770 775 780	2340
aag cgc cag atc acc cag aac aca gat tac cgc tta aac ccc atg Lys Arg Gln Ile Thr Gln Asn Thr Asp Tyr Arg Leu Asn Pro Met 785 790 795	2385
tta aga aaa gcc tgt aaa gct gac att cct aaa ttc tgt cac ggt Leu Arg Lys Ala Cys Lys Ala Asp Ile Pro Lys Phe Cys His Gly 800 805 810	2430
atc ctg act aag gcc aag gat gat tca gaa tta gaa gga caa gtc Ile Leu Thr Lys Ala Lys Asp Asp Ser Glu Leu Glu Gly Gln Val 815 820 825	2475
atc tct tgc ctg aag ctg aga tat gct gac cag cgc ctg tct tca Ile Ser Cys Leu Lys Leu Arg Tyr Ala Asp Gln Arg Leu Ser Ser 830 835 840	2520
gac tgt gaa gac cag atc cga atc att atc cag gag tcc gcc ctg Asp Cys Glu Asp Gln Ile Arg Ile Ile Ile Gln Glu Ser Ala Leu 845 850 855	2565
gac tac cgc ctg gat cct cag ctc cag ctg cac tgc tca gac gag Asp Tyr Arg Leu Asp Pro Gln Leu Gln Leu His Cys Ser Asp Glu 860 865 870	2610
atc tcc agt cta tgt gct gaa gaa gca gca gcc caa gag cag aca Ile Ser Ser Leu Cys Ala Glu Glu Ala Ala Ala Gln Glu Gln Thr 875 880 885	2655
ggc cag gtg gag gag tgc ctc aag gtc aac ctg ctc aag atc aaa Gly Gln Val Glu Glu Cys Leu Lys Val Asn Leu Leu Lys Ile Lys 890 895 900	2700
aca gaa ttg tgt aaa aag gaa gtg cta aac atg ctg aag gaa agc Thr Glu Leu Cys Lys Lys Glu Val Leu Asn Met Leu Lys Glu Ser 905 910 915	2745
aaa gca gac atc ttt gtt gac ccg gta ctt cat act gct tgt gcc Lys Ala Asp Ile Phe Val Asp Pro Val Leu His Thr Ala Cys Ala 920 925 930	2790
ctg gac att aaa cac cac tgc gca gcc atc acc cct ggc cgc ggg Leu Asp Ile Lys His His Cys Ala Ala Ile Thr Pro Gly Arg Gly 935 940 945	2835
cgt caa atg tcc tgt ctc atg gaa gca ctg gag gat aag cgg gtg Arg Gln Met Ser Cys Leu Met Glu Ala Leu Glu Asp Lys Arg Val 950 955 960	2880
agg tta cag ccc gag tgc aaa aag cgc ctc aat gac cgg att gag Arg Leu Gln Pro Glu Cys Lys Lys Arg Leu Asn Asp Arg Ile Glu 965 970 975	2925

Fig. 10-4

atg tgg agt tac gca gca aag gtg gcc cca gca gat ggc ttc tct	2970
Met Trp Ser Tyr Ala Ala Lys Val Ala Pro Ala Asp Gly Phe Ser	
980 985 990	
gat ctt gcc atg caa gta atg acg tct cca tct aag aac tac att	3015
Asp Leu Ala Met Gln Val Met Thr Ser Pro Ser Lys Asn Tyr Ile	
995 1000 1005	
ctc tct gtg atc agt ggg agc atc tgt ata ttg ttc ctg att ggc	3060
Leu Ser Val Ile Ser Gly Ser Ile Cys Ile Leu Phe Leu Ile Gly	
1010 1015 1020	
ctg atg tgt gga cgg atc acc aag cga gtg aca cga gag ctg aag	3105
Leu Met Cys Gly Arg Ile Thr Lys Arg Val Thr Arg Glu Leu LysA	
1025 1030 1035	
gac agg tag	
Asp Arg ***	
1038	

Fig. 10-5

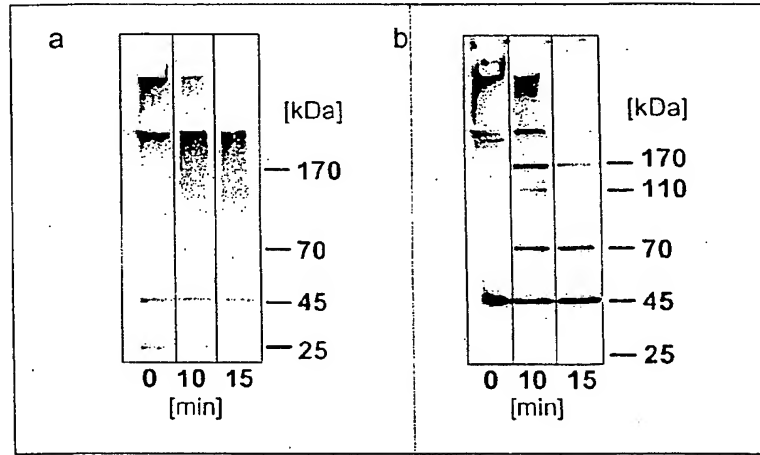


Fig. 11

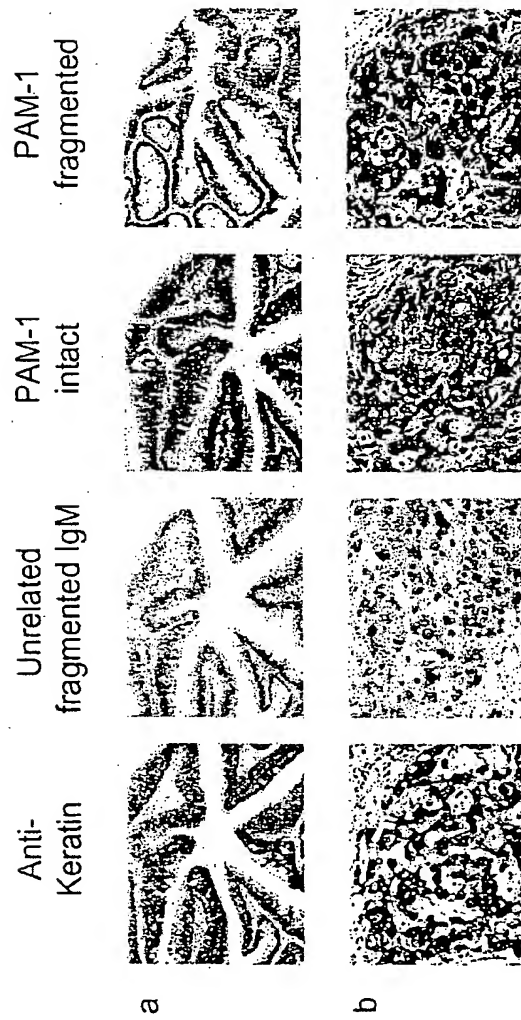


Fig. 12

Fig. 13

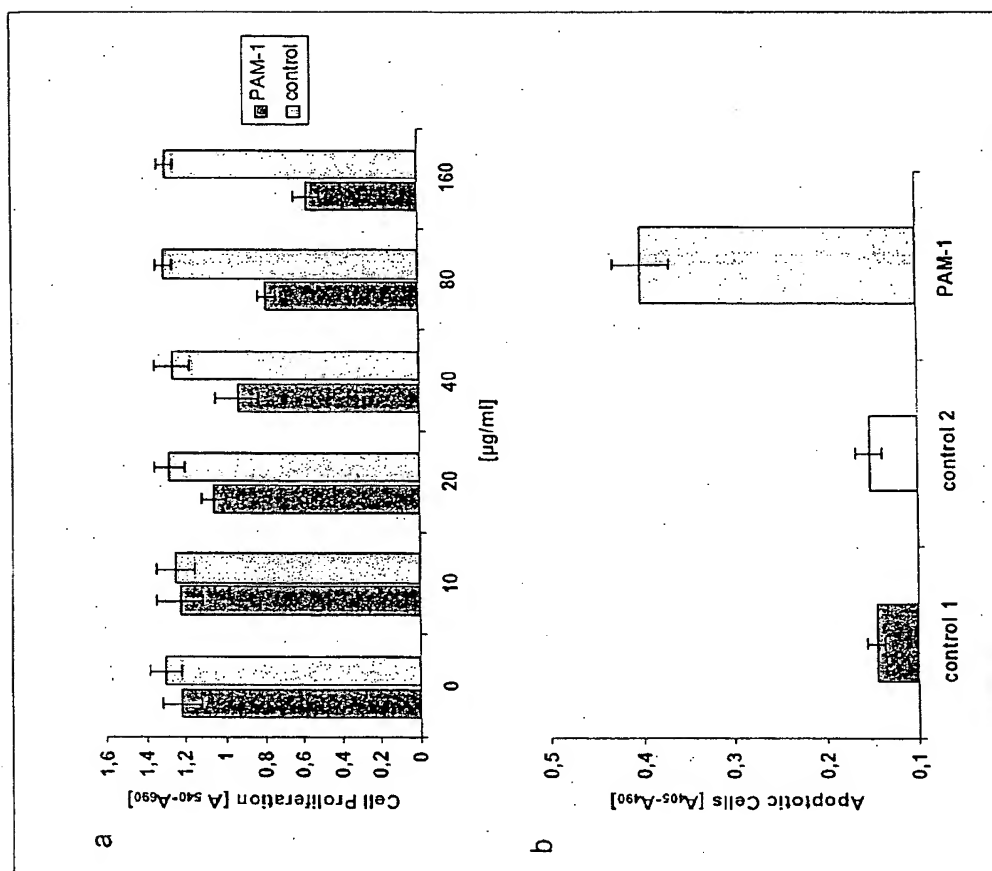
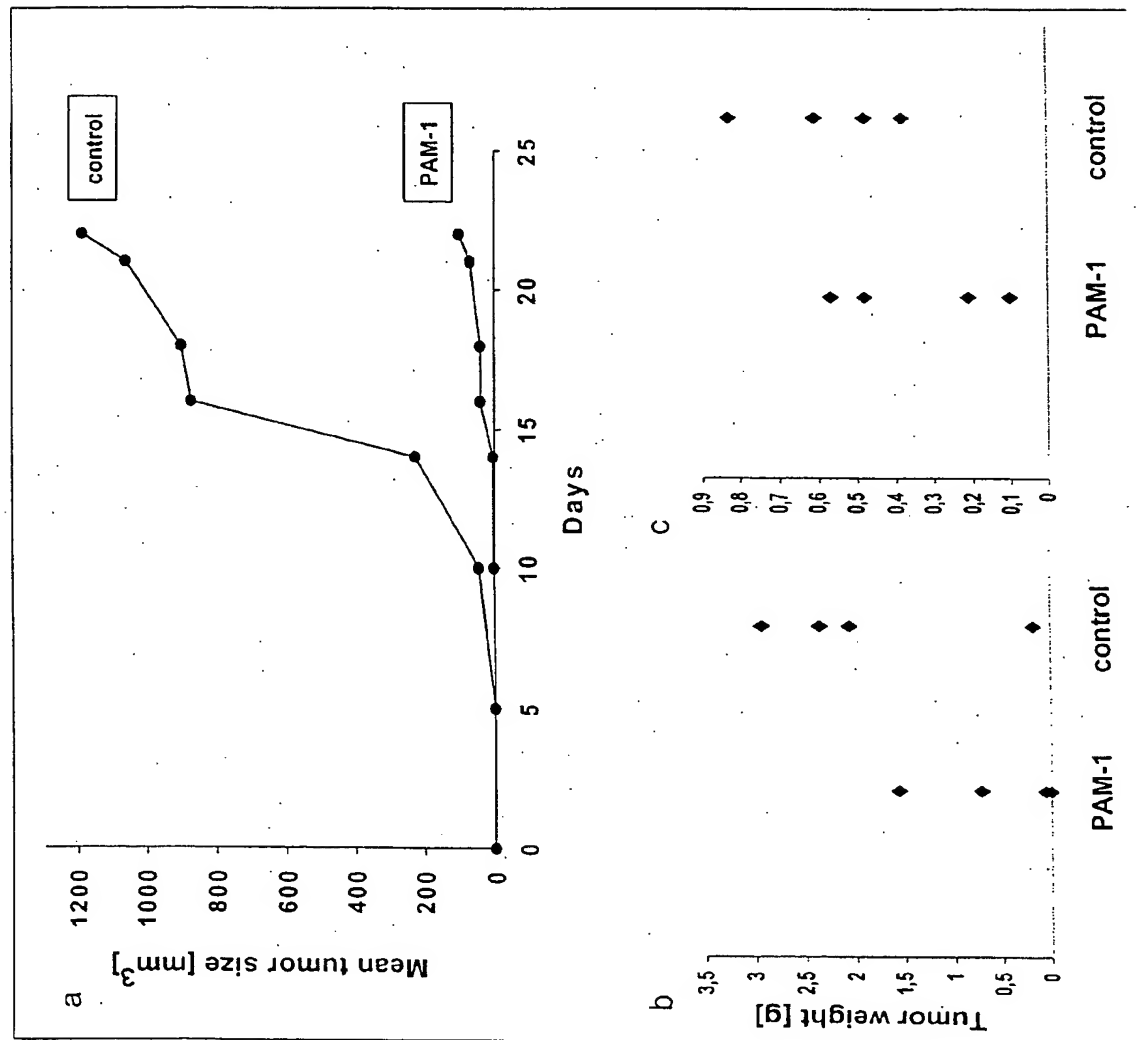




Fig. 14



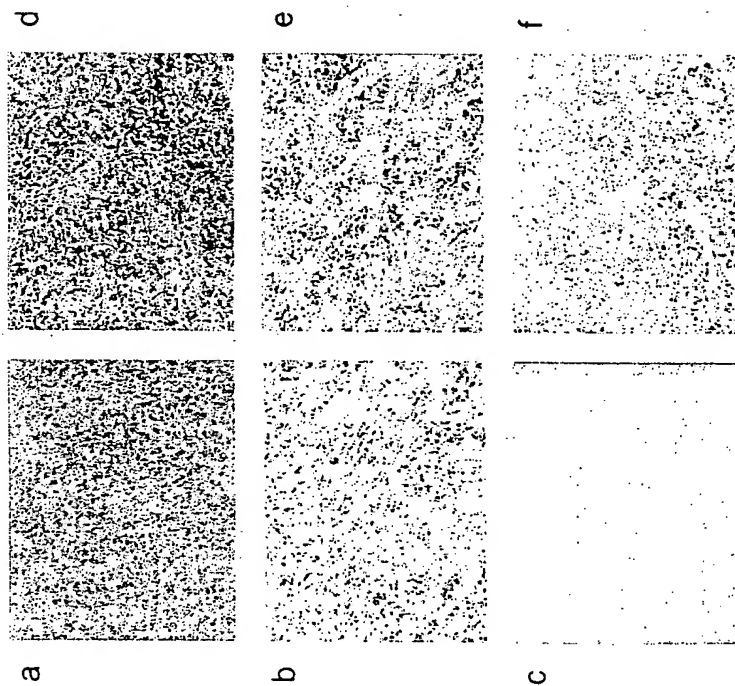


Fig. 15

23132	CFR-1	MG160	1	MAACGVRIRM	FLRAALHIL	LLFRAGGRNS	PARASHOGQ	GCANFVSEV	GOAGGGPAG	QQLPOLPOSS	OLQOQOQOQ	QOQOQPPQP	PFAGGPP-R
			1	MAACGVRIRM	FLRAALHIL	LLFRAGGRNS	PARASHOGQ	GCANFVSEV	GOAGGGPAG	QQLPOLPOSS	OLQOQOQOQ	QOQOQPPQP	PFAGGPP-R
			1	MAACGVRIRM	FLRAALHIL	LLFRAGGRNS	PARASHOGQ	GCANFVSEV	GOAGGGPAG	QQLPOLPOSS	OLQOQOQOQ	QOQOQPPQP	PFAGGPP-R
23132	CFR-1	MG160	101	RGAGAGGGW	KLAEEESCRE	DVTRVCPIIT	WSNNLAVLEC	LQDVREPENE	ISSDCHHLLM	NYKUNLTDD	KFESVAREVC	KSTITEIKEC	ADEPVCKGYN
			101	RGAGAGGGW	KLAEEESCRE	DVTRVCPIIT	WSNNLAVLEC	LQDVREPENE	ISSDCHHLLM	NYKUNLTDD	KFESVAREVC	KSTITEIKEC	ADEPVCKGYN
			101	RGAGAGGGW	KLAEEESCRE	DVTRVCPIIT	WSNNLAVLEC	LQDVREPENE	ISSDCHHLLM	NYKUNLTDD	KFESVAREVC	KSTITEIKEC	ADEPVCKGYN
23132	CFR-1	MG160	201	VSLVDHHRGN	ITEYQCHQYI	TKMTAIFSD	YLLICGFMDD	CKNDINILKC	GSTRIGEKDA	HSQGEVVSCL	EKGLVKEAEE	REPKIQVSEL	CKKAILLRVAE
			201	VSLVDHHRGN	ITEYQCHQYI	TKMTAIFSD	YLLICGFMDD	CKNDINILKC	GSTRIGEKDA	HSQGEVVSCL	EKGLVKEAEE	REPKIQVSEL	CKKAILLRVAE
			201	VSLVDHHRGN	ITEYQCHQYI	TKMTAIFSD	YLLICGFMDD	CKNDINILKC	GSTRIGEKDA	HSQGEVVSCL	EKGLVKEAEE	REPKIQVSEL	CKKAILLRVAE
23132	CFR-1	MG160	301	LSSJDFHLDR	ILYFACRDDR	ERFCENTQAG	EGRVYKCLFN	HKFEESMSEK	CREALTTROK	L'AODYKVS	SLAKSCKSD	KKYRCNVENL	PRSRERLSY
			301	LSSJDFHLDR	ILYFACRDDR	ERFCENTQAG	EGRVYKCLFN	HKFEESMSEK	CREALTTROK	L'AODYKVS	SLAKSCKSD	KKYRCNVENL	PRSRERLSY
			301	LSSJDFHLDR	ILYFACRDDR	ERFCENTQAG	EGRVYKCLFN	HKFEESMSEK	CREALTTROK	L'AODYKVS	SLAKSCKSD	KKYRCNVENL	PRSRERLSY
23132	CFR-1	MG160	401	LLWCLSAVH	KGQVSSBQ	GEKLDYRRML	MEFSLSPFI	ILSCGEIEH	HCGLHKKGR	TLHCLMKVVR	GEKGLCHNC	QOALOTLQ	TDPGADYRID
			401	LLWCLSAVH	KGQVSSBQ	GEKLDYRRML	MEFSLSPFI	ILSCGEIEH	HCGLHKKGR	TLHCLMKVVR	GEKGLCHNC	QOALOTLQ	TDPGADYRID
			401	LLWCLSAVH	KGQVSSBQ	GEKLDYRRML	MEFSLSPFI	ILSCGEIEH	HCGLHKKGR	TLHCLMKVVR	GEKGLCHNC	QOALOTLQ	TDPGADYRID
23132	CFR-1	MG160	501	RAINEACESV	IQTACKHRS	GDPMLISCLM	EHLYTEKMAE	DCEHRLLELO	YFISRDWKL	PVLYRKQGD	ASRLCHTHGW	NETSEFMPOG	AVFSCLYRHA
			501	RAINEACESV	IQTACKHRS	GDPMLISCLM	EHLYTEKMAE	DCEHRLLELO	YFISRDWKL	PVLYRKQGD	ASRLCHTHGW	NETSEFMPOG	AVFSCLYRHA
			501	RAINEACESV	IQTACKHRS	GDPMLISCLM	EHLYTEKMAE	DCEHRLLELO	YFISRDWKL	PVLYRKQGD	ASRLCHTHGW	NETSEFMPOG	AVFSCLYRHA
23132	CFR-1	MG160	601	YRTEQGRRL	SRECRAEVOR	ILHQRAMDVK	LOPALQDKCL	IDLGKWCSEK	TETGOELEC	ILHQRAMDVK	LOPALQDKCL	IDLGKWCSEK	TETGOELEC
			601	YRTEQGRRL	SRECRAEVOR	ILHQRAMDVK	LOPALQDKCL	IDLGKWCSEK	TETGOELEC	ILHQRAMDVK	LOPALQDKCL	IDLGKWCSEK	TETGOELEC
			601	YRTEQGRRL	SRECRAEVOR	ILHQRAMDVK	LOPALQDKCL	IDLGKWCSEK	TETGOELEC	ILHQRAMDVK	LOPALQDKCL	IDLGKWCSEK	TETGOELEC
23132	CFR-1	MG160	701	QNFCHOVADN	QIDSGOLMEC	LIONKHOKDM	NEKCAIGVTH	FOLVQMKDPR	FSYKFMACK	EDVLKJCPNI	KKKVDVVICL	STTVRNDTLQ	EAKEHRVSLK
			701	QNFCHOVADN	QIDSGOLMEC	LIONKHOKDM	NEKCAIGVTH	FOLVQMKDPR	FSYKFMACK	EDVLKJCPNI	KKKVDVVICL	STTVRNDTLQ	EAKEHRVSLK
			701	QNFCHOVADN	QIDSGOLMEC	LIONKHOKDM	NEKCAIGVTH	FOLVQMKDPR	FSYKFMACK	EDVLKJCPNI	KKKVDVVICL	STTVRNDTLQ	EAKEHRVSLK
23132	CFR-1	MG160	801	CRQLRVZEL	EMTEDIRLEP	OLYEACKSDI	KNFCSAVQYG	NAQIIECLKE	NKQLSTRCH	QKVKLQETE	MWDELOYTL	NRVCKOMIKR	FCPEADSKTM
			801	CRQLRVZEL	EMTEDIRLEP	OLYEACKSDI	KNFCSAVQYG	NAQIIECLKE	NKQLSTRCH	QKVKLQETE	MWDELOYTL	NRVCKOMIKR	FCPEADSKTM
			801	CRQLRVZEL	EMTEDIRLEP	OLYEACKSDI	KNFCSAVQYG	NAQIIECLKE	NKQLSTRCH	QKVKLQETE	MWDELOYTL	NRVCKOMIKR	FCPEADSKTM
23132	CFR-1	MG160	901	LOCLKQKNS	ELMDPKCKOM	ITRKQITQNT	DYRLNPLMR	ACKADIPKFC	HGILTKAKOD	SELEGQVISC	LKLYADQRL	SSDCEDQIRI	IIQESALDYR
			901	LOCLKQKNS	ELMDPKCKOM	ITRKQITQNT	DYRLNPLMR	ACKADIPKFC	HGILTKAKOD	SELEGQVISC	LKLYADQRL	SSDCEDQIRI	IIQESALDYR
			901	LOCLKQKNS	ELMDPKCKOM	ITRKQITQNT	DYRLNPLMR	ACKADIPKFC	HGILTKAKOD	SELEGQVISC	LKLYADQRL	SSDCEDQIRI	IIQESALDYR
23132	CFR-1	MG160	1001	LOPOLQLHCS	DEISSICREE	AAAOEQTGQV	SECLKNVLLX	IKTELCKKEV	LNMLKESRAD	IFVDVULHTA	CALDIKHCA	ALTTPGRGQM	SCIMEALEDK
			1001	LOPOLQLHCS	DEISSICREE	AAAOEQTGQV	SECLKNVLLX	IKTELCKKEV	LNMLKESRAD	IFVDVULHTA	CALDIKHCA	ALTTPGRGQM	SCIMEALEDK
			1001	LOPOLQLHCS	DEISSICREE	AAAOEQTGQV	SECLKNVLLX	IKTELCKKEV	LNMLKESRAD	IFVDVULHTA	CALDIKHCA	ALTTPGRGQM	SCIMEALEDK
23132	CFR-1	MG160	1101	RVALQPECKK	RLNDR-EMWS	YAAKVPADG	FSDLAMQVMT	SPSKNYILSV	ISGS-CILFL	IGLMCGRITK	RVTRLEKOR		
			1101	RVALQPECKK	RLNDR-EMWS	YAAKVPADG	FSDLAMQVMT	SPSKNYILSV	ISGS-CILFL	IGLMCGRITK	RVTRLEKOR		
			1101	RVALQPECKK	RLNDR-EMWS	YAAKVPADG	FSDLAMQVMT	SPSKNYILSV	ISGS-CILFL	IGLMCGRITK	RVTRLEKOR		

Fig. 16

Human antibody PAM-1 (clone 103/51)

Heavy chain sequence

CDR I																		
AGG	TCC	CTG	AGA	CTC	TCC	TGT	GCA	GCC	TCT	GGA	TTC	ACC	TTC	AGT	AGC	TAT	GGC	54
Arg	Ser	Leu	Arg	Leu	Ser	Cys	Ala	Ala	Ser	Gly	Phe	Thr	Phe	Ser	Ser	Tyr	Gly	
				5					10					15				
ATG	CAC	TGG	GTC	CGC	CAG	GCT	CCA	GGC	AAG	GGG	CTG	GAG	TGG	GTG	GCA	GTT	ATA	108
Met	His	Trp	Val	Arg	Gln	Ala	Pro	Gly	Lys	Gly	Leu	Glu	Trp	Val	Ala	Val	Ile	
	20					25					30					35		
CDR II																		
TCA	TAT	GAT	GGA	AGT	AAT	AAA	TAC	TAT	GCA	GAC	TCC	GTG	AAG	GGC	CGA	TTC	ACC	162
Ser	Tyr	Asp	Gly	Ser	Asn	Lys	Tyr	Tyr	Ala	Asp	Ser	Val	Lys	Gly	Arg	Phe	Thr	
			40					45					50					
ATC	TCC	AGA	GAC	AAT	TCC	AAG	AAC	ACG	CTG	TAT	CTG	CAA	ATG	AAC	AGC	CTG	AGA	216
Ile	Ser	Arg	Asp	Asn	Ser	Lys	Asn	Thr	Leu	Tyr	Leu	Gln	Met	Asn	Ser	Leu	Arg	
55					60				65					70				
CDR III																		
GCT	GAG	GAC	ACG	GCT	GTG	TAT	TAC	TGT	GCG	AGG	TCG	ACT	ACG	AGG	TCT	TAT	CCT	270
Ala	Glu	Asp	Thr	Ala	Val	Tyr	Tyr	Cys	Ala	Arg	Ser	Thr	Thr	Arg	Ser	Tyr	Pro	
		75					80					85					90	
CDR III																		
CTA	TAC	GGT	ATG	GAC	GTT	TGG	GGC	CAA	GGG	AAC	CCT	GTC	ACC					312
Leu	Tyr	Gly	Met	Asp	Val	Trp	Gly	Gln	Gly	Asn	Pro	Val	Thr					
				95					100									

Fig. 17

Human antibody PAM-1 (clone 103/51)Light chain sequence

GTG	ACC	TCC	TAT	GTG	CTG	ACT	CAG	CCA	CCC	TCG	GTG	TCA	GTG	GCC	CCA	GGA	CAG	54
Val	Thr	Ser	Tyr	Val	Leu	Thr	Gln	Pro	Pro	Ser	Val	Ser	Val	Ala	Pro	Gly	Gln	
				5					10					15				
CDR I																		
ACG	GCC	AGT	ATT	ACC	TGT	GGG	GGA	AAT	AAC	ATT	GGA	AGT	AAA	AGT	GTG	CAC	TGG	108
Thr	Ala	Ser	Ile	Thr	Cys	Gly	Gly	Asn	Asn	Ile	Gly	Ser	Lys	Ser	Val	His	Trp	
	20					25					30					35		
CDR II																		
TAC	CAT	CAG	AAG	CCA	GGC	CAG	GCC	CCT	GTG	CTG	GTC	GTC	TAT	GAT	GAT	AGC	GAC	162
Tyr	His	Gln	Lys	Pro	Gly	Gln	Ala	Pro	Val	Leu	Val	Val	Tyr	Asp	Asp	Ser	Asp	
			40					45					50					
CGG	CCC	TCA	GGG	ATC	CCT	GAG	CGA	TTC	TCT	GGC	TCC	AAC	TCT	GGG	AAC	ACG	GCC	216
Arg	Pro	Ser	Gly	Ile	Pro	Glu	Arg	Phe	Ser	Gly	Ser	Asn	Ser	Gly	Asn	Thr	Ala	
	55				60					65				70				
ACC	CTG	ACC	ATC	ACC	AGG	GTC	GAA	GCC	GGG	GAT	GAG	GCC	GAC	TAT	TAC	TGT	CAG	270
Thr	Leu	Thr	Ile	Thr	Arg	Val	Glu	Ala	Gly	Asp	Glu	Ala	Asp	Tyr	Tyr	Cys	Gln	
		75					80				85						90	
CDR III																		
GTG	TGG	GAT	AGT	AGT	AGT	GAT	CTC	AAT	TGG	GTG	TTC	GGC	GGA	AGG	ACC	CAA	GCT	324
Val	Trp	Asp	Ser	Ser	Ser	Asp	Leu	Asn	Trp	Val	Phe	Gly	Gly	Arg	Thr	Gln	Ala	
				95					100					105				
GAC	CGT	CCT	ACG	TCA	GCC	CAA	GGC	TGC	CCC	TCC	GGT	CAC	TCT	GTT	CCC	CGC	CCC	378
Asp	Arg	Pro	Thr	Ser	Ala	Gln	Gly	Cys	Pro	Ser	Gly	His	Ser	Val	Pro	Arg	Pro	
	110					115					120					125		
CCT	CTG	AAG	AGC	TTC	AAG	CTT												399
Pro	Leu	Lys	Ser	Phe	Lys	Leu												
						130												

Fig. 18